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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/973,322

DATE: 10/30/2001
TIME: 15:33:49

Input Set : A:\SEQLISTDYOU17001CP1.TXT
Output Set: N:\CRF3\10302001\I973322.raw

ENTERED

2.

4 <110> APPLICANT: Hope, Ralph Graham
5 McLauchlan, John
7 <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
10 <130> FILE REFERENCE: DYOU17.001CP1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/973,322
C--> 12 <141> CURRENT FILING DATE: 2001-10-09
12 <150> PRIOR APPLICATION NUMBER: US 09/201,916
13 <151> PRIOR FILING DATE: 1998-12-01
15 <150> PRIOR APPLICATION NUMBER: GB 9825951.8
16 <151> PRIOR FILING DATE: 1998-11-26
18 <160> NUMBER OF SEQ ID NOS: 20
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 630
24 <212> TYPE: DNA
25 <213> ORGANISM: Hepatitis C Virus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (43)...(630)
31 <400> SEQUENCE: 1
32 ggtgcttgcg agtgcccgag gaggctcgat agaccgtgca cc atg agc acg aat 54
33 33 Met Ser Thr Asn
34 34 1
35 cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102
36 Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
37 37 5 10 15 20
38 40 gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150
41 Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
42 42 25 30 35
43 ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198
44 Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
45 45 40 45 50
46 48 tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246
49 Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
50 50 55 60 65
52 cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294
53 Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
54 54 70 75 80
56 ctc tat ggc aat gag ggt tgc ggg tgg ggc tgg ctc ctg tcc ccc 342
57 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
58 58 85 90 95 100
60 agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg 390
61 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Ser
62 62 105 110 115
64 cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat 438
65 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
66 66 120 125 130

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68 ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc 486
69 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
70 135 140 145
72 agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat 534
73 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
74 150 155 160
76 gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc 582
77 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
78 165 170 175 180
80 ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac 630
81 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
82 185 190 195
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 60
88 <212> TYPE: DNA
89 <213> ORGANISM: Hepatitis C Virus
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)...(60)
94 <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
96 <400> SEQUENCE: 2
97 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48
98 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
99 1 5 10 15 60
101 ggc gcc cct ctt
102 Gly Ala Pro Leu
103 20
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 18
108 <212> TYPE: DNA
109 <213> ORGANISM: Hepatitis C Virus
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (1)...(18)
114 <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
116 <400> SEQUENCE: 3
117 ggt gtg aac tat gca aca 18
118 Gly Val Asn Tyr Ala Thr
119 1 5
122 <210> SEQ ID NO: 4
123 <211> LENGTH: 1900
124 <212> TYPE: DNA
125 <213> ORGANISM: Human
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (1)...(1900)
130 <223> OTHER INFORMATION: n = A,T,C or G
132 <400> SEQUENCE: 4
133 cgtcttcggg acgcggccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag 60

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134 gaagaaaaat ggcatccgtt gcagttgatc cacaaccgag tgggtgact cgggtggta 120
 135 acctgccctt ggtgagctcc acgtatgacc tcattgtcctc agcctatctc agtacaaagg 180
 136 accagtatcc ctacctaag tctgtgtgt agatgscaga gaacgggtgt aagaccatca 240
 137 cctccgtggc catgaccagt gctctgccc tcattccagaa gctagagccg caaattgcag 300
 138 ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
 139 atcagccatc aactcagatt gttgccaatg ccaaaggcgc tggacttggg gcaaaagatg 420
 W--> 140 ctgtgacgac tactgtgact ggggccaagg attctgtngc cagcacgatc acagggggtga 480
 141 tggacaagac caaaggggca gtactggca gtgtggagaa gaccaagtct gtggtcagt 540
 142 gcagcattaa cacagtctt gggagtcgga tgatgcgt cgtgacgt ggcgtagaaa 600
 143 atgcactcac caaatcagag ctgttggtag aacagtaccc cctctcaact gaggagaac 660
 144 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggt tcagaaggca agtattatg 720
 145 ttagactggg atccctgtct accaagcttc actccctgtc ctaccacgag gctctcagca 780
 146 gggtaaaaaga agctaagcaa aaaagccaaac agaccatttc tcagctccat tctactgttc 840
 147 acctgattga atttgcagg aagaatgtgt atagtccaa tcagaaaatt cagatgctc 900
 148 aggataagct ctacccctca tggtagagt gggaaaggag cattggatgatgatactg 960
 149 atgagtcctt ctgtgctgag cacattgagt cacgtactct tgcaatttgcg cgcacactt 1020
 150 ctcagcactt ccagaccacg tgccacaccc tcctgtccaa catccaagggt gtaccacaga 1080
 151 acatccaaga tcaagccaaag cacatgggg tgatggcagg cgacatctac tcagtttcc 1140
 152 gcaatgctgc ctcccttaaa gaagtgtctg acgcctcct cacttcttagc aaggggcagc 1200
 153 tgcagaaaat gaaggaaatct ttagatgacg tgatggatta tcttgttaac aacacgcggcc 1260
 154 tcaactggct ggttagtccc ttttacccctc agctgactga gtctcagaat gctcaggacc 1320
 155 aaggtgcaga gatggacaag agcagccagg agacccagcg atctgagcat aaaactcatt 1380
 156 aaacctgccc ctatcactag tgcattgtt ggcagacag atgacacatt ttgttatgtt 1440
 157 gaaattaaact tgcttagcaa ccctaaattt ggaagcaagt agcttagata aagccctca 1500
 158 attgttagttt tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
 159 ctgttccactt ggttaaaaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
 160 aaaattcaaa tgcacttatg ttctcattt atggccattt tggtgcctt gttactgttt 1680
 161 gtattgaata aaaacatctt catgtggct gggtagaaa ctgggtctg ctctgggtgt 1740
 162 atctgaaaag gcgttccac tgctttatct catgtgctt gcttgtaaaa ctgtattta 1800
 163 gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaatca ctgcaggata 1860
 W--> 164 gaccagtttaa gnageaaaca nncangtaca cnnaaganac 1900
 166 <210> SEQ ID NO: 5
 167 <211> LENGTH: 437
 168 <212> TYPE: PRT
 169 <213> ORGANISM: Human
 171 <220> FEATURE:
 172 <221> NAME/KEY: VARIANT
 173 <222> LOCATION: (1)...(437)
 174 <223> OTHER INFORMATION: Xaa = Any Amino Acid
 176 <400> SEQUENCE: 5
 177 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
 178 1 5 10 15
 179 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
 180 20 25 30
 181 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
 182 35 40 45
 W--> 183 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
 184 50 55 60
 185 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp

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186 65 70 75 80
 187 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
 188 85 90 95
 189 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
 190 100 105 110
 191 Thr Gly Ala Lys Asp Ala Val Thr Thr Val Thr Gly Ala Lys Asp
 192 115 120 125
 193 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
 194 130 135 140
 195 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
 196 145 150 155 160
 197 Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
 198 165 170 175
 199 Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
 200 180 185 190
 201 Leu Thr Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
 202 195 200 205
 203 Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
 204 210 215 220
 205 Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
 206 225 230 235 240
 207 Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
 208 245 250 255
 209 Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
 210 260 265 270
 211 Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
 212 275 280 285
 213 Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
 214 290 295 300
 215 His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
 216 305 310 315 320
 217 Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
 218 325 330 335
 219 Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
 220 340 345 350
 221 Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
 222 355 360 365
 223 Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
 224 370 375 380
 225 Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
 226 385 390 395 400
 227 Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
 228 405 410 415
 229 Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
 230 420 425 430
 231 Glu His Lys Thr His
 232 435
 235 <210> SEQ ID NO: 6
 236 <211> LENGTH: 31

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Input Set : A:\SEQLISTDYOU17001CP1.TXT
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237 <212> TYPE: PRT
 238 <213> ORGANISM: Artificial Sequence
 240 <220> FEATURE:
 241 <223> OTHER INFORMATION: branched peptide containing residues 5-27 of HCV
 242 core protein
 244 <221> NAME/KEY: VARIANT
 245 <222> LOCATION: (1)...(31)
 246 <223> OTHER INFORMATION: Xaa = Ala or Pro at position 1, and Ile or Asn at
 247 position 12
 249 <400> SEQUENCE: 6
 W--> 250 Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln
 251 1 5 10 15
 252 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
 253 20 25 30
 256 <210> SEQ ID NO: 7
 257 <211> LENGTH: 11
 258 <212> TYPE: DNA
 259 <213> ORGANISM: Artificial Sequence
 261 <220> FEATURE:
 262 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 263 protein deletion plasmids
 265 <400> SEQUENCE: 7
 266 gctgagatct a 11
 268 <210> SEQ ID NO: 8
 269 <211> LENGTH: 29
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Artificial Sequence
 273 <220> FEATURE:
 274 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 275 protein deletion plasmids
 277 <400> SEQUENCE: 8
 278 gtaacccttcc tggtttgctct tgagatcta 29
 280 <210> SEQ ID NO: 9
 281 <211> LENGTH: 17
 282 <212> TYPE: DNA
 283 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 286 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 287 protein deletion plasmids
 289 <400> SEQUENCE: 9
 290 gtaaccctttg agatcta 17
 292 <210> SEQ ID NO: 10
 293 <211> LENGTH: 18
 294 <212> TYPE: DNA
 295 <213> ORGANISM: Artificial Sequence
 297 <220> FEATURE:
 298 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
 299 protein deletion plasmids
 301 <400> SEQUENCE: 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/973,322

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Input Set : A:\SEQLISTDYOU17001CP1.TXT
Output Set: N:\CRF3\10302001\I973322.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6